

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Yu, Guo-Liang
Ni, Jian
Dixit, Vishva
Gentz, Reiner L.
Dillon, Patrick J.
- (ii) TITLE OF INVENTION: Death Domain Containing Receptors
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
 - (B) STREET: 1100 New York Ave., NW, Suite 600
 - (C) CITY: Washington
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: HEREWITH
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: Not Yet Assigned
 - (B) FILING DATE: 06-FEB-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/028,711
 - (B) FILING DATE: 17-OCT-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/013,285
 - (B) FILING DATE: 12-MAR-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Steffe, Eric K.
 - (B) REGISTRATION NUMBER: 36,688
 - (C) REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-371-2600
 - (B) TELEFAX: 202-371-2540

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1783 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: both

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(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 198..1481
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CATGGGTGGG	GGTGGGGGCG	CTGCTGGATT	CCTGCTCTGG	TGGAGGGGAA	ACTTGTGAGG		60									
GGCTGGTAAG	CGCCCCCTCC	GAAGCCTGGT	GTGTGCGCGG	GGGGAAGGAA	GTTAGTTTCC		120									
TCTCCACCCA	TGGGCACCCC	TTCTGCCCCG	GGCCTGGGAA	GTGGGCTGCT	CTGTGGGCAA		180									
ATGCTGGGGC	CTCTGAA	ATG	GAG	GAG	ACG	CAG	CAG	GGA	GAG	GCC	CCA	CGT	230			
		Met	Glu	Glu	Thr	Gln	Gln	Gly	Glu	Ala	Pro	Arg				
		1				5					10					
GGG	CAG	CTG	CGC	GGA	GAG	TCA	GCA	GCA	CCT	GTC	CCC	CAG	GCG	CTC	CTC	278
Gly	Gln	Leu	Arg	Gly	Glu	Ser	Ala	Ala	Pro	Val	Pro	Gln	Ala	Leu	Leu	
			15					20					25			
CTG	GTG	CTG	CTG	GGG	GCC	CGG	GCC	CAG	GGC	GGC	ACT	CGT	AGC	CCC	AGG	326
Leu	Val	Leu	Leu	Gly	Ala	Arg	Ala	Gln	Gly	Gly	Thr	Arg	Ser	Pro	Arg	
			30					35				40				
TGT	GAC	TGT	GCC	GGT	GAC	TTC	CAC	AAG	AAG	ATT	GGT	CTG	TTT	TGT	TGC	374
Cys	Asp	Cys	Ala	Gly	Asp	Phe	His	Lys	Lys	Ile	Gly	Leu	Phe	Cys	Cys	
			45					50				55				
AGA	GGC	TGC	CCA	GCG	GGG	CAC	TAC	CTG	AAG	GCC	CCT	TGC	ACG	GAG	CCC	422
Arg	Gly	Cys	Pro	Ala	Gly	His	Tyr	Leu	Lys	Ala	Pro	Cys	Thr	Glu	Pro	
			60			65				70					75	
TGC	GGC	AAC	TCC	ACC	TGC	CTT	GTG	TGT	CCC	CAA	GAC	ACC	TTC	TTG	GCC	470
Cys	Gly	Asn	Ser	Thr	Cys	Leu	Val	Cys	Pro	Gln	Asp	Thr	Phe	Leu	Ala	
				80					85					90		
TGG	GAG	AAC	CAC	CAT	AAT	TCT	GAA	TGT	GCC	CGC	TGC	CAG	GCC	TGT	GAT	518
Trp	Glu	Asn	His	His	Asn	Ser	Glu	Cys	Ala	Arg	Cys	Gln	Ala	Cys	Asp	
			95					100					105			
GAG	CAG	GCC	TCC	CAG	GTG	GCG	CTG	GAG	AAC	TGT	TCA	GCA	GTG	GCC	GAC	566
Glu	Gln	Ala	Ser	Gln	Val	Ala	Leu	Glu	Asn	Cys	Ser	Ala	Val	Ala	Asp	
			110				115					120				

ACC	CGC	TGT	GGC	TGT	AAG	CCA	GGC	TGG	TTT	GTG	GAG	TGC	CAG	GTC	AGC	614
Thr	Arg	Cys	Gly	Cys	Lys	Pro	Gly	Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	
125						130				135						
CAA	TGT	GTC	AGC	AGT	TCA	CCC	TTC	TAC	TGC	CAA	CCA	TGC	CTA	GAC	TGC	662
Gln	Cys	Val	Ser	Ser	Ser	Pro	Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	
140					145					150					155	
GGG	GCC	CTG	CAC	CGC	CAC	ACA	CGG	CTA	CTC	TGT	TCC	CGC	AGA	GAT	ACT	710
Gly	Ala	Leu	His	Arg	His	Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	Asp	Thr	
				160					165						170	
GAC	TGT	GGG	ACC	TGC	CTG	CCT	GGC	TTC	TAT	GAA	CAT	GGC	GAT	GGC	TGC	758
Asp	Cys	Gly	Thr	Cys	Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Gly	Cys	
			175					180					185			
GTG	TCC	TGC	CCC	ACG	AGC	ACC	CTG	GGG	AGC	TGT	CCA	GAG	CGC	TGT	GCC	806
Val	Ser	Cys	Pro	Thr	Ser	Thr	Leu	Gly	Ser	Cys	Pro	Glu	Arg	Cys	Ala	
		190					195					200				
GCT	GTC	TGT	GGC	TGG	AGG	CAG	ATG	TTC	TGG	GTC	CAG	GTG	CTC	CTG	GCT	854
Ala	Val	Cys	Gly	Trp	Arg	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Ala	
205						210					215					
GGC	CTT	GTG	GTC	CCC	CTC	CTG	CTT	GGG	GCC	ACC	CTG	ACC	TAC	ACA	TAC	902
Gly	Leu	Val	Val	Pro	Leu	Leu	Leu	Gly	Ala	Thr	Leu	Thr	Tyr	Thr	Tyr	
220					225					230					235	
CGC	CAC	TGC	TGG	CCT	CAC	AAG	CCC	CTG	GTT	ACT	GCA	GAT	GAA	GCT	GGG	950
Arg	His	Cys	Trp	Pro	His	Lys	Pro	Leu	Val	Thr	Ala	Asp	Glu	Ala	Gly	
				240					245					250		
ATG	GAG	GCT	CTG	ACC	CCA	CCA	CCG	GCC	ACC	CAT	CTG	TCA	CCC	TTG	GAC	998
Met	Glu	Ala	Leu	Thr	Pro	Pro	Pro	Ala	Thr	His	Leu	Ser	Pro	Leu	Asp	
			255					260					265			
AGC	GCC	CAC	ACC	CTT	CTA	GCA	CCT	CCT	GAC	AGC	AGT	GAG	AAG	ATC	TGC	1046
Ser	Ala	His	Thr	Leu	Leu	Ala	Pro	Pro	Asp	Ser	Ser	Glu	Lys	Ile	Cys	
		270					275					280				
ACC	GTC	CAG	TTG	GTG	GGT	AAC	AGC	TGG	ACC	CCT	GGC	TAC	CCC	GAG	ACC	1094
Thr	Val	Gln	Leu	Val	Gly	Asn	Ser	Trp	Thr	Pro	Gly	Tyr	Pro	Glu	Thr	
285						290					295					
CAG	GAG	GCG	CTC	TGC	CCG	CAG	GTG	ACA	TGG	TCC	TGG	GAC	CAG	TTG	CCC	1142
Gln	Glu	Ala	Leu	Cys	Pro	Gln	Val	Thr	Trp	Ser	Trp	Asp	Gln	Leu	Pro	
300					305					310					315	
AGC	AGA	GCT	CTT	GGC	CCC	GCT	GCT	GCG	CCC	ACA	CTC	TCG	CCA	GAG	TCC	1190
Ser	Arg	Ala	Leu	Gly	Pro	Ala	Ala	Ala	Pro	Thr	Leu	Ser	Pro	Glu	Ser	
			320					325						330		
CCA	GCC	GGC	TCG	CCA	GCC	ATG	ATG	CTG	CAG	CCG	GGC	CCG	CAG	CTC	TAC	1238
Pro	Ala	Gly	Ser	Pro	Ala	Met	Met	Leu	Gln	Pro	Gly	Pro	Gln	Leu	Tyr	
			335					340					345			

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GAC GTG ATG GAC GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC Asp Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg 350 355 360	1286
ACG CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG GAG ATC Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile 365 370 375	1334
GGC CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC AAG CGC TGG CGC CAG Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln 380 385 390 395	1382
CAG CAG CCC GCG GGC CTC GGA GCC GTT TAC GCG GCC CTG GAG CGC ATG Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met 400 405 410	1430
GGG CTG GAC GGC TGC GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly 415 420 425	1478
CCG TGACACGGCG CCCACTTGCC ACCTAGGCGC TCTGGTGGCC CTTGCAGAAG Pro	1531
CCCTAAGTAC GGTTACTTAT GCGTGTAGAC ATTTTATGTC ACTTATTAAG CCGCTGGCAC	1591
GGCCCTGCGT AGCAGCACCA GCCGGCCCCA CCCCTGCTCG CCCCTATCGC TCCAGCCAAG	1651
GCGAAGAAGC ACGAACGAAT GTCGAGAGGG GGTGAAGACA TTTCTCAACT TCTCGGCCGG	1711
AGTTTGGCTG AGATCGCGGT ATTAAATCTG TGAAAGAAAA CAAAACAAAA CAAAAAAAAA	1771
AAAAAAAAAA AA	1783

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Glu Thr Gln Gln Gly Glu Ala Pro Arg Gly Gln Leu Arg Gly 1 5 10 15
Glu Ser Ala Ala Pro Val Pro Gln Ala Leu Leu Leu Val Leu Leu Gly 20 25 30
Ala Arg Ala Gln Gly Gly Thr Arg Ser Pro Arg Cys Asp Cys Ala Gly 35 40 45

Asp	Phe	His	Lys	Lys	Ile	Gly	Leu	Phe	Cys	Cys	Arg	Gly	Cys	Pro	Ala	
50						55					60					
Gly	His	Tyr	Leu	Lys	Ala	Pro	Cys	Thr	Glu	Pro	Cys	Gly	Asn	Ser	Thr	
65					70					75						80
Cys	Leu	Val	Cys	Pro	Gln	Asp	Thr	Phe	Leu	Ala	Trp	Glu	Asn	His	His	
				85					90					95		
Asn	Ser	Glu	Cys	Ala	Arg	Cys	Gln	Ala	Cys	Asp	Glu	Gln	Ala	Ser	Gln	
			100					105					110			
Val	Ala	Leu	Glu	Asn	Cys	Ser	Ala	Val	Ala	Asp	Thr	Arg	Cys	Gly	Cys	
			115				120					125				
Lys	Pro	Gly	Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	Gln	Cys	Val	Ser	Ser	
130						135					140					
Ser	Pro	Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	Gly	Ala	Leu	His	Arg	
145					150					155					160	
His	Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	Asp	Thr	Asp	Cys	Gly	Thr	Cys	
				165					170					175		
Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Gly	Cys	Val	Ser	Cys	Pro	Thr	
			180					185					190			
Ser	Thr	Leu	Gly	Ser	Cys	Pro	Glu	Arg	Cys	Ala	Ala	Val	Cys	Gly	Trp	
			195				200					205				
Arg	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Ala	Gly	Leu	Val	Val	Pro	
210						215					220					
Leu	Leu	Leu	Gly	Ala	Thr	Leu	Thr	Tyr	Thr	Tyr	Arg	His	Cys	Trp	Pro	
225					230					235					240	
His	Lys	Pro	Leu	Val	Thr	Ala	Asp	Glu	Ala	Gly	Met	Glu	Ala	Leu	Thr	
				245					250					255		
Pro	Pro	Pro	Ala	Thr	His	Leu	Ser	Pro	Leu	Asp	Ser	Ala	His	Thr	Leu	
			260					265					270			
Leu	Ala	Pro	Pro	Asp	Ser	Ser	Glu	Lys	Ile	Cys	Thr	Val	Gln	Leu	Val	
			275				280					285				
Gly	Asn	Ser	Trp	Thr	Pro	Gly	Tyr	Pro	Glu	Thr	Gln	Glu	Ala	Leu	Cys	
290						295					300					
Pro	Gln	Val	Thr	Trp	Ser	Trp	Asp	Gln	Leu	Pro	Ser	Arg	Ala	Leu	Gly	
305					310					315					320	
Pro	Ala	Ala	Ala	Pro	Thr	Leu	Ser	Pro	Glu	Ser	Pro	Ala	Gly	Ser	Pro	
				325					330					335		
Ala	Met	Met	Leu	Gln	Pro	Gly	Pro	Gln	Leu	Tyr	Asp	Val	Met	Asp	Ala	

(2) INFORMATION FOR SEQ ID NO:3:

(A) LENGTH: 1254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..1251

ATG	GAG	CAG	CGG	CCG	CGG	GGC	TGC	GCG	GCG	GTG	GCG	GCG	GCG	CTC	CTC	48
Met	Glu	Gln	Arg	Pro	Arg	Gly	Cys	Ala	Ala	Val	Ala	Ala	Ala	Leu	Leu	
	430					435					440					
CTG	GTG	CTG	CTG	GGG	GCC	CGG	GCC	CAG	GGC	GGC	ACT	CGT	AGC	CCC	AGG	96
Leu	Val	Leu	Leu	Gly	Ala	Arg	Ala	Gln	Gly	Gly	Thr	Arg	Ser	Pro	Arg	
	445				450					455					460	
TGT	GAC	TGT	GCC	GGT	GAC	TTC	CAC	AAG	AAG	ATT	GGT	CTG	TTT	TGT	TGC	144
Cys	Asp	Cys	Ala	Gly	Asp	Phe	His	Lys	Lys	Ile	Gly	Leu	Phe	Cys	Cys	
				465					470					475		
AGA	GGC	TGC	CCA	GCG	GGG	CAC	TAC	CTG	AAG	GCC	CCT	TGC	ACG	GAG	CCC	192
Arg	Gly	Cys	Pro	Ala	Gly	His	Tyr	Leu	Lys	Ala	Pro	Cys	Thr	Glu	Pro	
			480					485					490			
TGC	GGC	AAC	TCC	ACC	TGC	CTT	GTG	TGT	CCC	CAA	GAC	ACC	TTC	TTG	GCC	240
Cys	Gly	Asn	Ser	Thr	Cys	Leu	Val	Cys	Pro	Gln	Asp	Thr	Phe	Leu	Ala	
		495					500					505				

TGG	GAG	AAC	CAC	CAT	AAT	TCT	GAA	TGT	GCC	CGC	TGC	CAG	GCC	TGT	GAT	288
Trp	Glu	Asn	His	His	Asn	Ser	Glu	Cys	Ala	Arg	Cys	Gln	Ala	Cys	Asp	
510						515					520					
GAG	CAG	GCC	TCC	CAG	GTG	GCG	CTG	GAG	AAC	TGT	TCA	GCA	GTG	GCC	GAC	336
Glu	Gln	Ala	Ser	Gln	Val	Ala	Leu	Glu	Asn	Cys	Ser	Ala	Val	Ala	Asp	
525					530				535					540		
ACC	CGC	TGT	GGC	TGT	AAG	CCA	GGC	TGG	TTT	GTG	GAG	TGC	CAG	GTC	AGC	384
Thr	Arg	Cys	Gly	Cys	Lys	Pro	Gly	Trp	Phe	Val	Glu	Cys	Gln	Val	Ser	
			545					550						555		
CAA	TGT	GTC	AGC	AGT	TCA	CCC	TTC	TAC	TGC	CAA	CCA	TGC	CTA	GAC	TGC	432
Gln	Cys	Val	Ser	Ser	Ser	Pro	Phe	Tyr	Cys	Gln	Pro	Cys	Leu	Asp	Cys	
		560					565						570			
GGG	GCC	CTG	CAC	CGC	CAC	ACA	CGG	CTA	CTC	TGT	TCC	CGC	AGA	GAT	ACT	480
Gly	Ala	Leu	His	Arg	His	Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	Asp	Thr	
	575					580						585				
GAC	TGT	GGG	ACC	TGC	CTG	CCT	GGC	TTC	TAT	GAA	CAT	GGC	GAT	GGC	TGC	528
Asp	Cys	Gly	Thr	Cys	Leu	Pro	Gly	Phe	Tyr	Glu	His	Gly	Asp	Gly	Cys	
	590					595				600						
GTG	TCC	TGC	CCC	ACG	AGC	ACC	CTG	GGG	AGC	TGT	CCA	GAG	CGC	TGT	GCC	576
Val	Ser	Cys	Pro	Thr	Ser	Thr	Leu	Gly	Ser	Cys	Pro	Glu	Arg	Cys	Ala	
605					610					615				620		
GCT	GTC	TGT	GGC	TGG	AGG	CAG	ATG	TTC	TGG	GTC	CAG	GTG	CTC	CTG	GCT	624
Ala	Val	Cys	Gly	Trp	Arg	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Ala	
			625					630					635			
GGC	CTT	GTG	GTC	CCC	CTC	CTG	CTT	GGG	GCC	ACC	CTG	ACC	TAC	ACA	TAC	672
Gly	Leu	Val	Val	Pro	Leu	Leu	Leu	Gly	Ala	Thr	Leu	Thr	Tyr	Thr	Tyr	
		640				645							650			
CGC	CAC	TGC	TGG	CCT	CAC	AAG	CCC	CTG	GTT	ACT	GCA	GAT	GAA	GCT	GGG	720
Arg	His	Cys	Trp	Pro	His	Lys	Pro	Leu	Val	Thr	Ala	Asp	Glu	Ala	Gly	
		655				660						665				
ATG	GAG	GCT	CTG	ACC	CCA	CCA	CCG	GCC	ACC	CAT	CTG	TCA	CCC	TTG	GAC	768
Met	Glu	Ala	Leu	Thr	Pro	Pro	Pro	Ala	Thr	His	Leu	Ser	Pro	Leu	Asp	
	670				675						680					
AGC	GCC	CAC	ACC	CTT	CTA	GCA	CCT	CCT	GAC	AGC	AGT	GAG	AAG	ATC	TGC	816
Ser	Ala	His	Thr	Leu	Leu	Ala	Pro	Pro	Asp	Ser	Ser	Glu	Lys	Ile	Cys	
685					690				695					700		
ACC	GTC	CAG	TTG	GTG	GGT	AAC	AGC	TGG	ACC	CCT	GGC	TAC	CCC	GAG	ACC	864
Thr	Val	Gln	Leu	Val	Gly	Asn	Ser	Trp	Thr	Pro	Gly	Tyr	Pro	Glu	Thr	
			705					710					715			
CAG	GAG	GCG	CTC	TGC	CCG	CAG	GTG	ACA	TGG	TCC	TGG	GAC	CAG	TTG	CCC	912
Gln	Glu	Ala	Leu	Cys	Pro	Gln	Val	Thr	Trp	Ser	Trp	Asp	Gln	Leu	Pro	
		720						725					730			

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AGC AGA GCT CTT GGC CCC GCT GCT GCG CCC ACA CTC TCG CCA GAG TCC	960
Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr Leu Ser Pro Glu Ser	
735 740 745	
CCA GCC GGC TCG CCA GCC ATG ATG CTG CAG CCG GGC CCG CAG CTC TAC	1008
Pro Ala Gly Ser Pro Ala Met Met Leu Gln Pro Gly Pro Gln Leu Tyr	
750 755 760	
GAC GTG ATG GAC GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC	1056
Asp Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg	
765 770 775 780	
ACG CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG GAG ATC	1104
Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu Ile	
785 790 795	
GGC CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC AAG CGC TGG CGC CAG	1152
Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp Arg Gln	
800 805 810	
CAG CAG CCC GCG GGC CTC GGA GCC GTT TAC GCG GCC CTG GAG CGC ATG	1200
Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu Glu Arg Met	
815 820 825	
GGG CTG GAC GGC TGC GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC	1248
Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly	
830 835 840	
CCG TGA	1254
Pro	
845	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Glu	Gln	Arg	Pro	Arg	Gly	Cys	Ala	Ala	Val	Ala	Ala	Ala	Leu	Leu
1				5				10						15	
Leu	Val	Leu	Leu	Gly	Ala	Arg	Ala	Gln	Gly	Gly	Thr	Arg	Ser	Pro	Arg
		20						25						30	
Cys	Asp	Cys	Ala	Gly	Asp	Phe	His	Lys	Lys	Ile	Gly	Leu	Phe	Cys	Cys
		35					40					45			
Arg	Gly	Cys	Pro	Ala	Gly	His	Tyr	Leu	Lys	Ala	Pro	Cys	Thr	Glu	Pro
		50				55					60				

Cys 65	Gly	Asn	Ser	Thr	Cys 70	Leu	Val	Cys	Pro	Gln	Asp	Thr	Phe	Leu	Ala 80
Trp	Glu	Asn	His	His 85	Asn	Ser	Glu	Cys	Ala 90	Arg	Cys	Gln	Ala	Cys 95	Asp
Glu	Gln	Ala	Ser	Gln 100	Val	Ala	Leu	Glu	Asn 105	Cys	Ser	Ala	Val	Ala 110	Asp
Thr	Arg	Cys 115	Gly	Cys	Lys	Pro	Gly 120	Trp	Phe	Val	Glu	Cys 125	Gln	Val	Ser
Gln	Cys 130	Val	Ser	Ser	Ser	Pro 135	Phe	Tyr	Cys	Gln 140	Pro	Cys	Leu	Asp	Cys
Gly 145	Ala	Leu	His	Arg	His 150	Thr	Arg	Leu	Leu	Cys 155	Ser	Arg	Arg	Asp	Thr 160
Asp	Cys	Gly	Thr	Cys 165	Leu	Pro	Gly	Phe	Tyr 170	Glu	His	Gly	Asp	Gly 175	Cys
Val	Ser	Cys	Pro 180	Thr	Ser	Thr	Leu	Gly 185	Ser	Cys	Pro	Glu	Arg 190	Cys	Ala
Ala	Val 195	Cys	Gly	Trp	Arg	Gln	Met 200	Phe	Trp	Val	Gln	Val 205	Leu	Leu	Ala
Gly 210	Leu	Val	Val	Pro	Leu	Leu 215	Leu	Gly	Ala	Thr	Leu 220	Thr	Tyr	Thr	Tyr
Arg 225	His	Cys	Trp	Pro	His 230	Lys	Pro	Leu	Val	Thr 235	Ala	Asp	Glu	Ala	Gly 240
Met	Glu	Ala	Leu	Thr 245	Pro	Pro	Pro	Ala	Thr 250	His	Leu	Ser	Pro	Leu 255	Asp
Ser	Ala	His	Thr 260	Leu	Leu	Ala	Pro	Pro 265	Asp	Ser	Ser	Glu	Lys 270	Ile	Cys
Thr	Val 275	Gln	Leu	Val	Gly	Asn	Ser 280	Trp	Thr	Pro	Gly	Tyr 285	Pro	Glu	Thr
Gln 290	Glu	Ala	Leu	Cys	Pro	Gln 295	Val	Thr	Trp	Ser	Trp 300	Asp	Gln	Leu	Pro
Ser 305	Arg	Ala	Leu	Gly	Pro 310	Ala	Ala	Ala	Pro	Thr 315	Leu	Ser	Pro	Glu	Ser 320
Pro	Ala	Gly	Ser	Pro 325	Ala	Met	Met	Leu	Gln 330	Pro	Gly	Pro	Gln	Leu 335	Tyr
Asp	Val	Met 340	Asp	Ala	Val	Pro	Ala	Arg 345	Arg	Trp	Lys	Glu 350	Phe	Val	Arg
Thr	Leu	Gly	Leu	Arg	Glu	Ala	Glu	Ile	Glu	Ala	Val	Glu	Val	Glu	Ile

Pro

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Gly	Leu	Ser	Thr	Val	Pro	Asp	Leu	Leu	Leu	Pro	Leu	Val	Leu	Leu
1				5				10						15	
Glu	Leu	Leu	Val	Gly	Ile	Tyr	Pro	Ser	Gly	Val	Ile	Gly	Leu	Val	Pro
			20					25					30		
His	Leu	Gly	Asp	Arg	Glu	Lys	Arg	Asp	Ser	Val	Cys	Pro	Gln	Gly	Lys
		35					40					45			
Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	Ile	Cys	Cys	Thr	Lys	Cys	His	Lys
	50					55					60				
Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp
65					70					75					80
Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu
				85					90					95	
Arg	His	Cys	Leu	Ser	Cys	Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val
			100					105					110		
Glu	Ile	Ser	Ser	Cys	Thr	Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg
		115					120					125			
Lys	Asn	Gln	Tyr	Arg	His	Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe
	130					135					140				

Asn 145	Cys	Ser	Leu	Cys	Leu	Asn	Gly	Thr	Val	His	Leu	Ser	Cys	Gln	Glu
150					155					160					
Lys	Gln	Asn	Thr	Val	Cys	Thr	Cys	His	Ala	Gly	Phe	Phe	Leu	Arg	Glu
165					170					175					
Asn	Glu	Cys	Val	Ser	Cys	Ser	Asn	Cys	Lys	Lys	Ser	Leu	Glu	Cys	Thr
180					185					190					
Lys	Leu	Cys	Leu	Pro	Gln	Ile	Glu	Asn	Val	Lys	Gly	Thr	Glu	Asp	Ser
195					200					205					
Gly	Thr	Thr	Val	Leu	Leu	Pro	Leu	Val	Ile	Phe	Phe	Gly	Leu	Cys	Leu
210					215					220					
Leu	Ser	Leu	Leu	Phe	Ile	Gly	Leu	Met	Tyr	Arg	Tyr	Gln	Arg	Trp	Lys
225					230					235					
Ser	Lys	Leu	Tyr	Ser	Ile	Val	Cys	Gly	Lys	Ser	Thr	Pro	Glu	Lys	Glu
245					250					255					
Gly	Glu	Leu	Glu	Gly	Thr	Thr	Thr	Lys	Pro	Leu	Ala	Pro	Asn	Pro	Ser
260					265					270					
Phe	Ser	Pro	Thr	Pro	Gly	Phe	Thr	Pro	Thr	Leu	Gly	Phe	Ser	Pro	Val
275					280					285					
Pro	Ser	Ser	Thr	Phe	Thr	Ser	Ser	Ser	Thr	Tyr	Thr	Pro	Gly	Asp	Cys
290					295					300					
Pro	Asn	Phe	Ala	Ala	Pro	Arg	Arg	Glu	Val	Ala	Pro	Pro	Tyr	Gln	Gly
305					310					315					
Ala	Asp	Pro	Ile	Leu	Ala	Thr	Ala	Leu	Ala	Ser	Asp	Pro	Ile	Pro	Asn
325					330					335					
Pro	Leu	Gln	Lys	Trp	Glu	Asp	Ser	Ala	His	Lys	Pro	Gln	Ser	Leu	Asp
340					345					350					
Thr	Asp	Asp	Pro	Ala	Thr	Leu	Tyr	Ala	Val	Val	Glu	Asn	Val	Pro	Pro
355					360					365					
Leu	Arg	Trp	Lys	Glu	Phe	Val	Arg	Arg	Leu	Gly	Leu	Ser	Asp	His	Glu
370					375					380					
Ile	Asp	Arg	Leu	Glu	Leu	Gln	Asn	Gly	Arg	Cys	Leu	Arg	Glu	Ala	Gln
385					390					395					
Tyr	Ser	Met	Leu	Ala	Thr	Trp	Arg	Arg	Arg	Thr	Pro	Arg	Arg	Glu	Ala
405					410					415					
Thr	Leu	Glu	Leu	Leu	Gly	Arg	Val	Leu	Arg	Asp	Met	Asp	Leu	Leu	Gly
420					425					430					
Cys	Leu	Glu	Asp	Ile	Glu	Glu	Ala	Leu	Cys	Gly	Pro	Ala	Ala	Leu	Pro

445

(2) INFORMATION FOR SEO ID NO:6:

(A) LENGTH: 335 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Leu	Gly	Ile	Trp	Thr	Leu	Leu	Pro	Leu	Val	Leu	Thr	Ser	Val	Ala
1				5					10					15	
Arg	Leu	Ser	Ser	Lys	Ser	Val	Asn	Ala	Gln	Val	Thr	Asp	Ile	Asn	Ser
			20					25					30		
Lys	Gly	Leu	Glu	Leu	Arg	Lys	Thr	Val	Thr	Thr	Val	Glu	Thr	Gln	Asn
		35					40					45			
Leu	Glu	Gly	Leu	His	His	Asp	Gly	Gln	Phe	Cys	His	Lys	Pro	Cys	Pro
	50					55					60				
Pro	Gly	Glu	Arg	Lys	Ala	Arg	Asp	Cys	Thr	Val	Asn	Gly	Asp	Glu	Pro
65					70					75					80
Asp	Cys	Val	Pro	Cys	Gln	Glu	Gly	Lys	Glu	Tyr	Thr	Asp	Lys	Ala	His
				85					90					95	
Phe	Ser	Ser	Lys	Cys	Arg	Arg	Cys	Arg	Leu	Cys	Asp	Glu	Gly	His	Gly
			100					105					110		
Leu	Glu	Val	Glu	Ile	Asn	Cys	Thr	Arg	Thr	Gln	Asn	Thr	Lys	Cys	Arg
		115					120					125			
Cys	Lys	Pro	Asn	Phe	Phe	Gln	Asn	Ser	Thr	Val	Cys	Glu	His	Cys	Asp
		130				135					140				
Pro	Cys	Thr	Lys	Cys	Glu	His	Gly	Ile	Ile	Lys	Glu	Cys	Thr	Leu	Thr
145					150					155					160
Ser	Asn	Thr	Lys	Cys	Lys	Glu	Glu	Gly	Ser	Arg	Ser	Asn	Leu	Gly	Trp
				165					170					175	
Leu	Cys	Leu	Leu	Leu	Leu	Pro	Ile	Pro	Leu	Ile	Val	Trp	Val	Lys	Arg
			180					185					190		

Lys	Glu	Val	Gln	Lys	Thr	Cys	Arg	Lys	His	Arg	Lys	Glu	Asn	Gln	Gly
		195					200					205			
Ser	His	Glu	Ser	Pro	Thr	Leu	Asn	Pro	Glu	Thr	Val	Ala	Ile	Asn	Leu
	210					215					220				
Ser	Asp	Val	Asp	Leu	Ser	Lys	Tyr	Ile	Thr	Thr	Ile	Ala	Gly	Val	Met
225				230					235					240	
Thr	Leu	Ser	Gln	Val	Lys	Gly	Phe	Val	Arg	Lys	Asn	Gly	Val	Asn	Glu
			245					250						255	
Ala	Lys	Ile	Asp	Glu	Ile	Lys	Asn	Asp	Asn	Val	Gln	Asp	Thr	Ala	Glu
			260					265					270		
Gln	Lys	Val	Gln	Leu	Leu	Arg	Asn	Trp	His	Gln	Leu	His	Gly	Lys	Lys
	275						280					285			
Glu	Ala	Tyr	Asp	Thr	Leu	Ile	Lys	Asp	Leu	Lys	Lys	Ala	Asn	Leu	Cys
	290					295					300				
Thr	Leu	Ala	Glu	Lys	Ile	Gln	Thr	Ile	Ile	Leu	Lys	Asp	Ile	Thr	Ser
305				310						315					320
Asp	Ser	Glu	Asn	Ser	Asn	Phe	Arg	Asn	Glu	Ile	Gln	Ser	Leu	Val	
			325					330						335	

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGCCATGGG GGCCCGGCGG CAG

23

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

667511647160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGAAGCTTC TAGGACCCAG AACATCTGCC

30

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCGGATCCG CCATCATGGA GGAGACGCAG CAG

33

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGGATCCG CCATCATGGA GCAGCGGCCG CGG

33

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGTCTAGAT CAAAGCGTAG TCTGGGACGT CGTATGGGTA CGGGCCGCGC TGCA

54

CGCGGATCCG

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCGGATCCG CCATCATGGA GGAGACGCAG CAG

33

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGCGGATCCG CCATCATGGA GCAGCGGCCG CGG

33

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGCGGATCCT CACGGGCCGC GCTGCA

26

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCGGATCCG CCATCATGGA GGAGACGCAG CAG

33

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCGGATCCG CCATCATGGA GCAGCGGCCG CGG

33

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCGAGATCTA GTCTGGACCC AGAACATCTG CCTCC

35

CGCGGATCCG CCATCATGGA GGAGACGCAG CAG